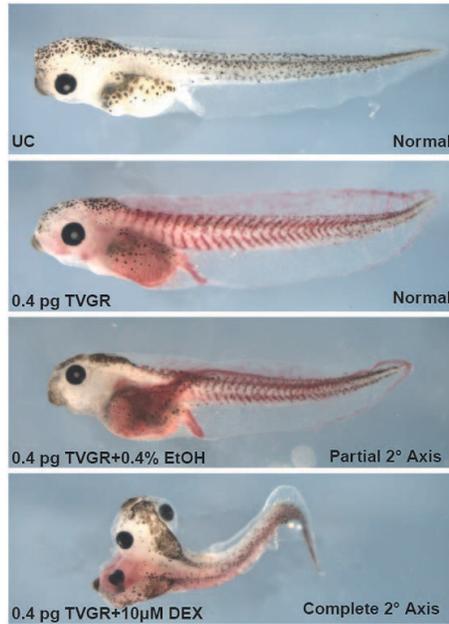
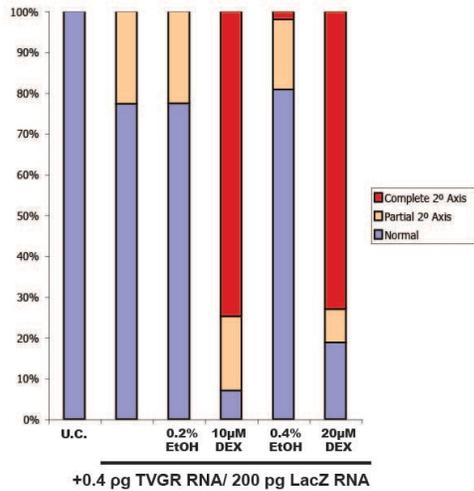


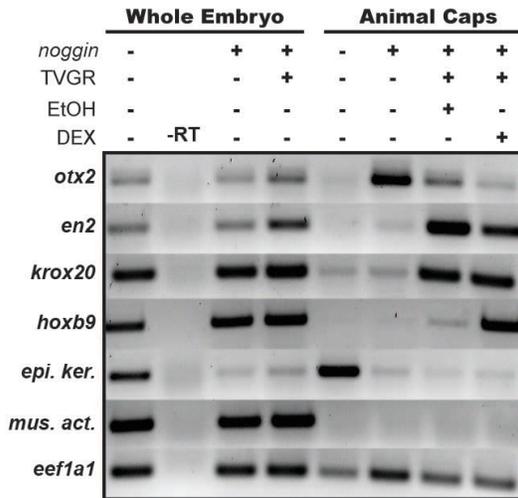
## Supplementary Material

**A**

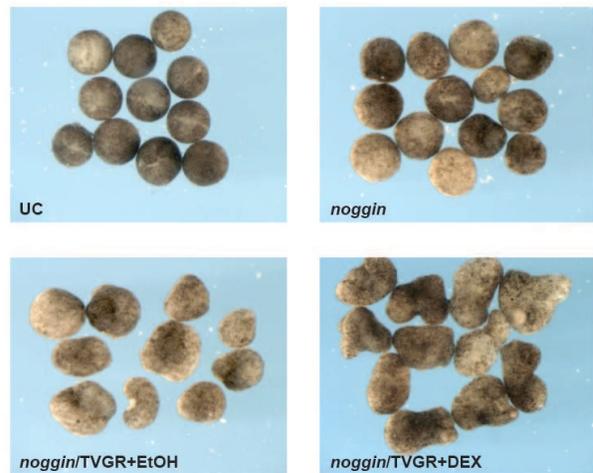
TVGR/Dex Induction of Wnt Signaling



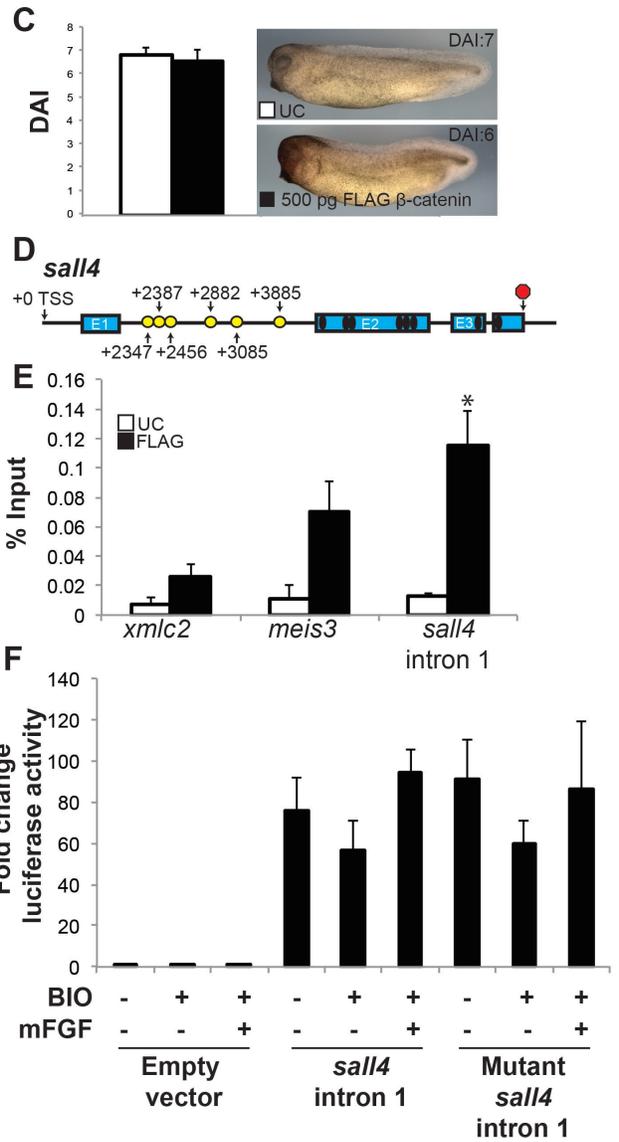
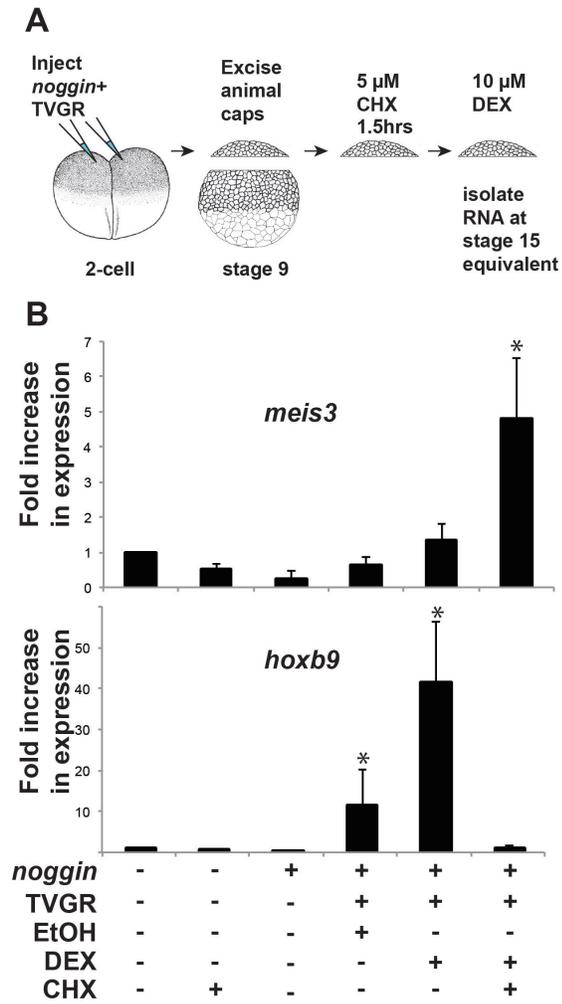
**B**



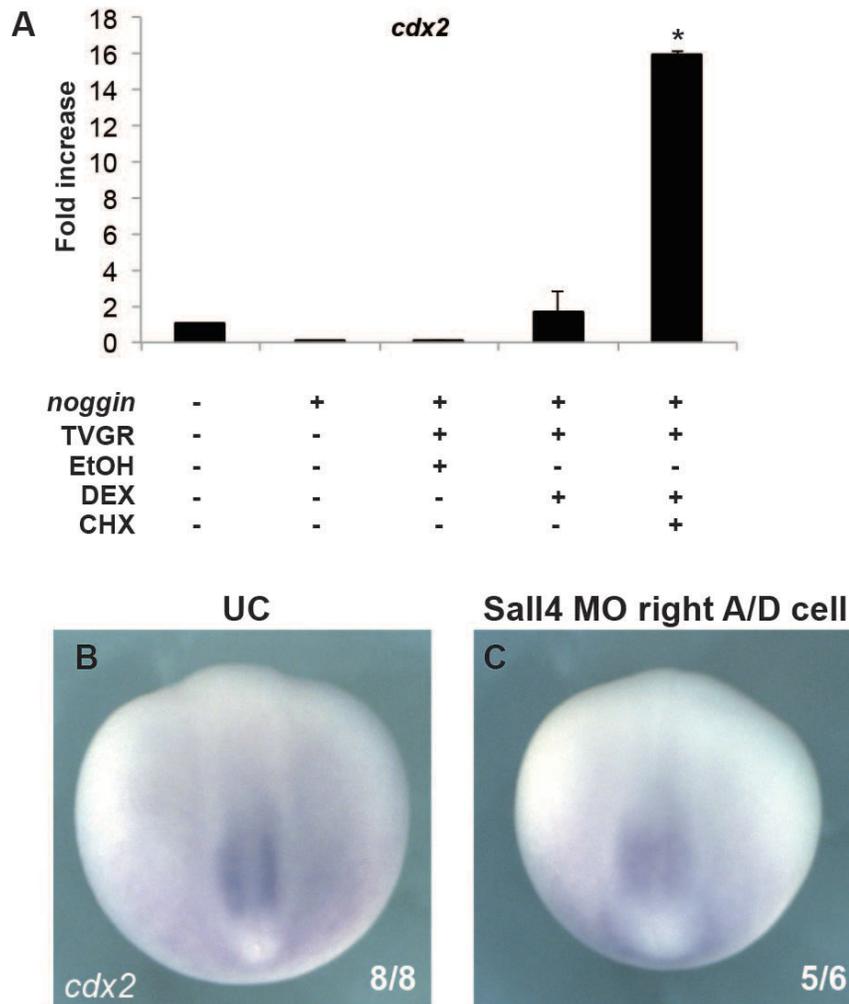
**C**



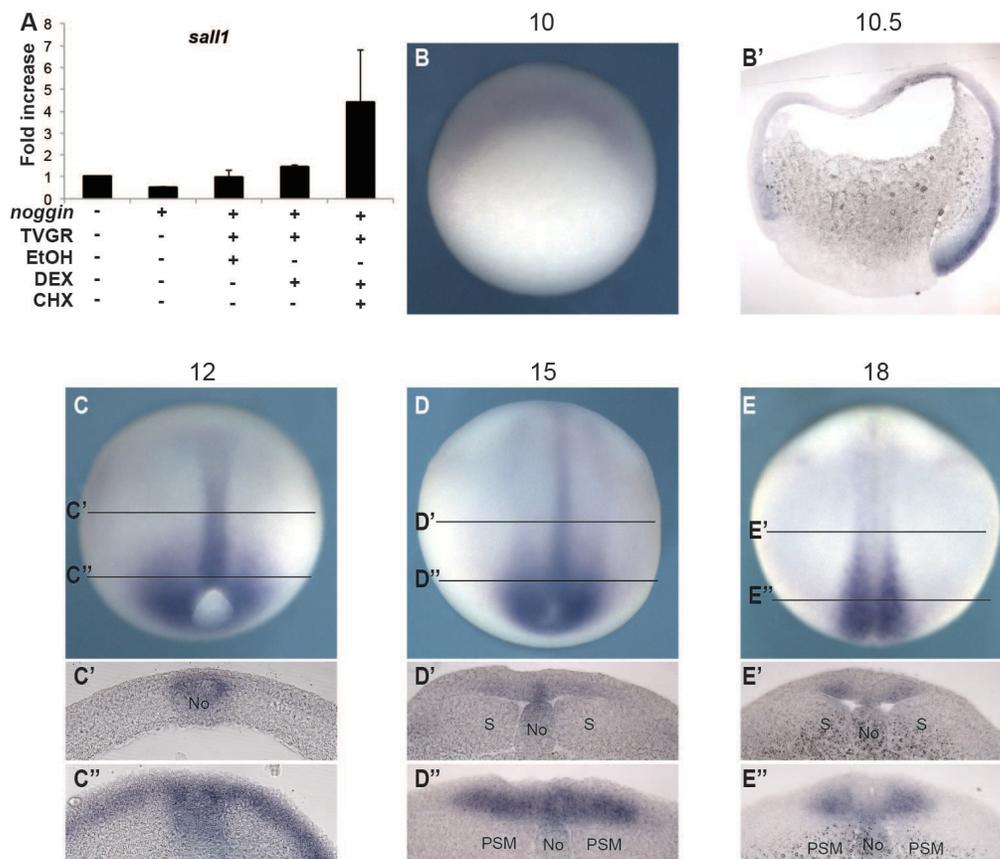
**Figure S1: TVGR activates canonical Wnt signaling.** (A) Quantification of secondary axis induction by ventral vegetal injection of TVGR at the 4-cell stage with representative tadpoles from each class. (B) RT-PCR on 5 whole embryos or 25 animal caps treated with the indicated reagents. -RT: reaction done in the absence of Reverse Transcriptase, *epi. ker.*: epidermal keratin (epidermis), *mus. act.*: muscle actin (mesoderm) (C) Animal caps treated with the indicated reagents.



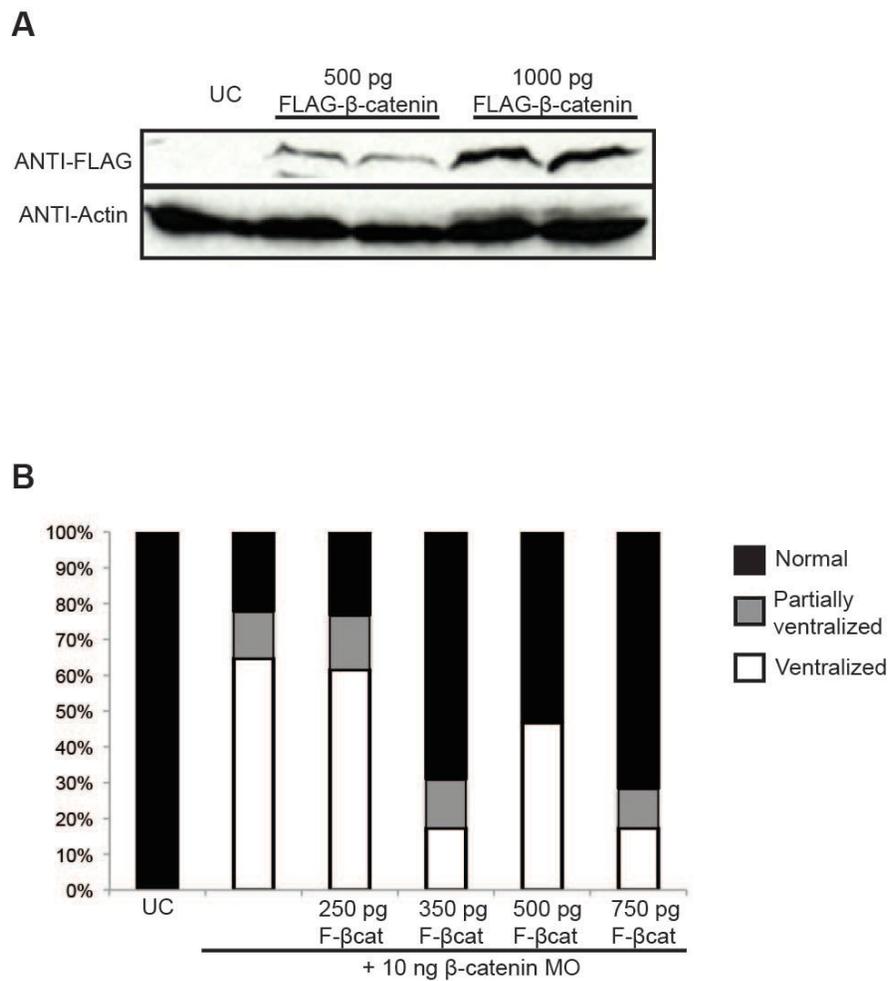
**Figure S2: Intron 1 of *sall4* binds  $\beta$ -catenin but does not mediate a Wnt signal.** (A) Using animal caps to screen for direct transcriptional targets of Wnt in neural tissue. (B) qPCR on 15-25 animal caps treated as indicated on the X-axis. The Y-axis shows expression relative to *odc*. *meis3* and *hoxb9* serve as controls for known direct and indirect targets of Wnt, respectively. (C) Quantification of dorsalization in uninjected embryos (open bars) and embryos injected anically with 500 pg FLAG-tagged  $\beta$ -catenin RNA (250 pg/blastomere) at the 2-cell stage (filled bars) as scored by the dorsoanterior index (DAI). Error bars: 1 SEM. Images show a representative uninjected (UC) embryo with a DAI of 7 (normal) and a representative embryo with a DAI of 6 (kinked axis). (D) Schematic of the genomic locus of *sall4* in *Xenopus laevis* (Xenbase.org). Blue boxes indicate exons and yellow circles indicate the location of putative TCF/LEF binding sites. Black ovals show the locations of the zinc-finger domains. Numbers indicate the position of putative binding sites relative to the transcription start site (TSS). (E) Chromatin immunoprecipitation of FLAG-tagged  $\beta$ -catenin in late gastrulae/early neurulae. Open bars represent uninjected embryos and closed bars represent embryos injected with 500 pg FLAG-tagged  $\beta$ -catenin (250 pg/blastomere at the 2-cell stage). Error bars: 1 SEM per cent input for each measurement. (F) Luciferase reporter assays in HEK293 cells treated with or without BIO and/or mouse FGF. Error bars: 1 SEM. All means were compared by one-way ANOVA followed by Tukey post-hoc analyses (\*:  $p < 0.05$ ).



**Figure S3: *cdx2* is activated by canonical Wnt signaling and not affected by Sall4 knockdown** (A) qPCR on 5 whole embryos or 15 to 25 animal caps treated according to the conditions indicated on the X-axis. The Y-axis shows expression relative to *odc*. Error bars: 1 SEM. (B-C) *cdx2* expression at stage 18. Dorsal views with the anterior oriented towards the top. (B) Uninjected control embryo. (C) Embryo injected with 20 ng Sall4 MO in one animal-dorsal cell at the 4-cell stage.



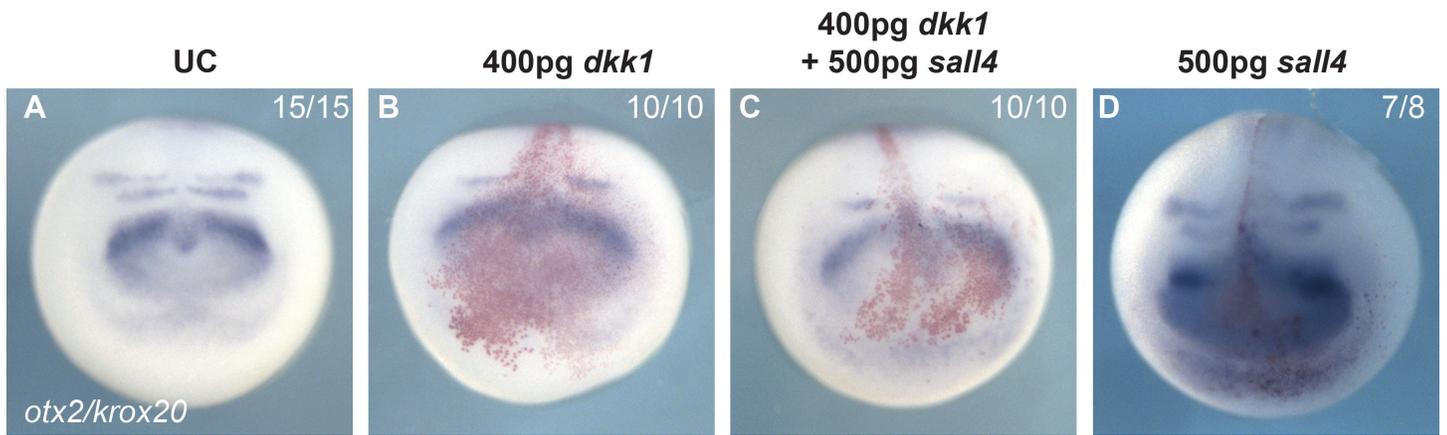
**Figure S4: *sall1* is activated by canonical Wnt signaling and expressed during early embryogenesis.** (A) qPCR on 5 whole embryos or 15 to 25 animal caps treated according to the conditions indicated on the X-axis. The Y-axis shows expression relative to *odc*. Error bars: 1 SEM. (B-E) Whole-mount *in situ* hybridizations of *sall1* in *Xenopus laevis* embryos. (B) Whole mount stage 10 embryo stained for *sall1*, dorso-vegetal view with the dorsal lip of the blastopore oriented towards the top. (B') Sagittal section of stage 10.5 embryo stained for *sall1* expression, animal pole is to the top and dorsal is to the right. (C-D) Dorsal views of indicated neurula stage embryos, anterior is oriented towards the top. (C'-C'') Transverse sections of stage 12 embryos stained for *sall1*, (C') anterior and (C'') posterior. (D'-D'') Transverse sections of stage 15 embryos stained for *sall1*, (D') anterior and (D'') posterior. (E'-E'') Transverse sections of stage 18 embryos stained for *sall1*, (E') anterior and (E'') posterior. (B', C'-E'') 50  $\mu$ M sections, (C'-E'') dorsal oriented towards the top. No: notochord, S: somite, PSM: presomitic mesoderm.



**Figure S5: Injected embryos express functional FLAG-tagged β-catenin.** (A) Western blot for the FLAG epitope in injected embryos. Actin serves as the loading control. (B) Ventralization of embryos injected with β-catenin MO and co-injection with FLAG-tagged β-catenin RNA. F-βcat: FLAG-tagged β-catenin.



TATTTAAATGAGATAAATATCTATCTCTCTATATCTCTAAAGAGAAATCACACCCTTTTTGAAGATTTTT  
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ATCACTGGGCATATACACGTGGAGGAGGCTTCCTTAACTGGTGGGTTTTCTTTAGCTAAGGGTCAGTTGGGAT  
TTGGATGCGGCGACTAGGTTAACACACAGTCCTTATCTGTTACAGGTGAAGGGTTAAACGAGGCCAACTGGT  
TTTTGTAGTTGTCCTTTTGTACAGTGTAAGGTGCCGGTGGGCCTGCTGGTATAACCTCTGGCTCCTTAGTGTG  
GTGGCAGGTTAATGTCAGGACTGATCCAGTAGGGTTTGTCCATTGCCAATTATGTGACTATTGGTGACCGATT  
TTGTTACCTCCGATCTGTTGTGGAGACCAGAAAGATTCTGATGATTTTTCTTTAGTGGTTTTGTCTTTTTAGAG  
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GGCCAGGCAGCTCTGAGTCAAGTGGGGTCCACATAATTTTTTTTTTTTTTTTTCATTAATTAAA**ATGTTTC**CATA  
CCTCCAATGCTGCCTTTTGCCTGGTGCAGGGAAGGATTTGTATAGAATATATGCCAGCTTAATGGCTGTACAGA  
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TCCCTCAGTGATCTTTGTGTAAATCCACGTGTAGTATTTACCATACATGTGCTGAGCACTAACACAGGATGAGT  
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CCCTCCCAATCCATTTGTTAGTGATTTAATCTAAACCCTGCTGACTTCACTGCATTCTTCTAACTTATTGGA  
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CGTTAACGCCGGTTATGCTCAGCTTGTGGAAACCACTGGAGGCCAACTTAAGATATTTTGCAGACATAAAATC  
AGACTCCTTAAAAGAGAGATGAATTAAGCTAGCCATAGACGTGCAGATTAGACAAACGAACGTCTTTTCCAAT  
ACTCTACCTGCAAATAACCATTTCAGATTAATATAAAGTTGCAAAGAGAACAATTTGCACGATCGGGCCATTTA  
TTGACTGGCGCAATCGTATGAAAGTTATGTTTGACAAACGGTAGTTACTGTCTCCCATTTGATAGCTGTAGCCG  
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CGTACAAAACTTTTTTCATGTGATCGTATCTGTGTGTCTAGGGCGGCGATGCGGGACATGATTTTGTATAGAATT  
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GTATCTTCTAGCAATGGTGAATCTGTTGGGTATAGGACCTGTAAGTTCATTAATTGGCCAAACAATATCTGGT  
TAACTTTTTTTTTTTTTAACTTTTACAG



**Figure S7: Sall4 does not rescue Dkk1-induced anteriorization.** (A-D) Anterior views of whole-mount *in situ* hybridizations for *otx2* and *krox20* on *Xenopus laevis* embryos. (A) Uninjected control (UC). (B) Embryo injected with 400pg *dkk1* RNA. (C) Embryo injected with 400pg *dkk1* and 500pg *sall4* RNA. (D) Embryo injected with 500pg *sall4* RNA.

**Table S1: List of all primers used.** RT-PCR: Conventional RT-PCR. qPCR: quantitative PCR. WMISH: Used to make a probe for whole mount *in situ* hybridization. ChIP: Used for qPCR on immunoprecipitated chromatin.

Gene	Forward	Reverse
<i>cdx2</i> (qPCR)	5'-ACATACCGGGATCCAAGACA-3'	5'-CAGCCTGAGTCTGCTGGATT-3'
<i>eefla1</i> (RT-PCR/qPCR)	5'-CCCTGCTGGAAGCTCTTGAC-3'	5'-GGACACCAGTCTCCACACGA-5'
<i>en2</i> (RT-PCR)	5'-CAGCCTGGGTCTACTGCAC-3'	5'-CTTTGCCTCCTCTGCTCAGT-3'
<i>epidermal keratin</i> (RT-PCR)	5'-GACCTGGAAGGGAAGATCC-3'	5'-GAAGAGCCAGCTCATTCTCAA-3'
<i>hoxb9</i> (qPCR)	5'-TACTTACGGGCTTGGCTGGA-3'	5'-AGCGTGTAACCAGTTGGCTG-3'
<i>hoxb9</i> (RT-PCR)	5'-CTCCAGCAGCCAAATTCTCT-3'	5'-CAGTTGGCTGAGGGGTTG-3'
<i>krox20</i> (RT-PCR)	5'-CCAGTGACTTTTGGTAGTTTGTG-3'	5'-TGGACGAGTAGGAGAAATCCA-3'
<i>meis3</i> (ChIP)	5'-CACTGTAAGTTATTGCCTCAAAGG-3'	5'-AGCTTGTAATACTTGTGGGCTTT-3'
<i>meis3</i> (qPCR)	5'-CAGGATACAGGGCTCACGAT-3'	5'-CTTGGGGCTGCTGTGTAATC-3'
<i>meis3</i> (RT-PCR)	5'-ATGATCGTGATGGCTCTTCC-3'	5'-CCCTGTGCGATTAGATTGGT-3'
<i>muscle actin</i> (RT-PCR)	5'-GACTCTGGGGATGGTGTGAC-3'	5'-AGCAGTGGCCATTTCATTCT-3'
<i>odc</i> (RT-PCR/qPCR)	5'-GGGCTGGATCGTATCGTAGA-3'	5'-TGCCAGTGTGGTCTTGACAT-3'
<i>otx2</i> (RT-PCR)	5'-TATCTCAAGCAACCGCCATA-3'	5'-AACCAAACCTGGACTCTGGA-3'
<i>pou25</i> (qPCR)	5'-GGGCCACCACTATCCCTAAT-3'	5'-GTGTGTAGCCCAGGGACACT-3'
<i>pou60</i> (qPCR)	5'-AGTTTGCCAAGGAGCTGAAA-3'	5'-GGACTCAAAGCGGCAGATAG-3'
<i>pou91</i> (qPCR)	5'-ACTTATTTGCCCGTCTCCT-3'	5'-CCCCATTGAGATCACTTGCT-3'
<i>sall1</i> (qPCR)	5'-GAGAGGGGTCAAATCCATCG-3'	5'-GGAGGTGGTGGATTTTCATT-3'
<i>sall1</i> (WMISH probe)	5'-CTTTCAAAGCATGGTGAGCA-3'	5'-ATGGCACGATGGACACTGTA-3'
<i>sall4</i> (qPCR)	5'-TGTCAAAGGATGAGCATTTCG-3'	5'-CATGCGGTCAGAGGGTACTT-3'
<i>sall4</i> (WMISH probe)	5'-CTTGGTGCGCACTTATCTCA-3'	5'-GCCTCAGATTGTGTGGGACT-3'
<i>sall4 intron 1</i> (ChIP)	5'-GGGAGTTGGAAGGTACAAAGC-3'	5'-AACCAAACAATAGACGAAAAATAAA-3'
<i>xmle2</i> (ChIP)	5'-TGGGATATTTACTGAACACAATG-3'	5'-CGTCCTGTGCCACCTAATG-3'

<b>Gene</b>	<b>Forward</b>	<b>Reverse</b>
<b>WT <i>sall4</i> intron 1</b> (Luciferase assay)	5'- CACTCCCTCCCCTTTATTC -3'	5'-CACTCCCTCCCCTTTATTC-3'
<b><i>sall4</i> intron 1 TCF/ LEF site +2347</b> (mutagenesis)	5'- GGAGTTGGAAGGTACGGG GCTACATATTG-3'	5'- CAATATGTAGCCCCGTACCTCC AACTCC-3'
<b><i>sall4</i> intron 1 TCF/ LEF site +2387</b> (mutagenesis)	5'- CATATGAACGGGGAGGTC GCCAATG-3'	5'- CATTGGCGACCTCCCCGTTTCATAT G-3'
<b><i>sall4</i> intron 1 TCF/ LEF site +2465</b> (mutagenesis)	5'- GGTTAATCTTTCGGGGACT TCCATTTAGTG-3'	5'- CACTAAATGGAAGTCCCCGAAA GATTAACC-3'

**Table S2: Genes with >2-fold expression (direct Wnt activation vs. anterior neural) found by RNA-Seq.**

The data represents fold increase as measured by fragments per kilobase of exon per million reads (FPKM).

The nature of this quantification can lead to high fold changes in lowly expressed genes and likely accounts for the massive fold increases calculated in genes with the highest differential expression.

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
hnRNP H3	gi 52138902 gb BC082630.1	1.51235E+11
H3 histone, family 3B	gi 27503243 gb BC042290.1	1.03963E+11
Glutamate ammonia ligase	gi 49256010 gb BC073448.1	39422399227
Protein phosphatase type 1 alpha, catalytic subunit	gi 27695193 gb BC041730.1	2824225487
Ki-67	gi 115527315 gb BC124560.1	1131777.541
copper chaperone for superoxide dismutase	gi 50418348 gb BC077488.1	3919.698435
FoxI4.2	gi 50418055 gb BC078036.1	1329.542265
Ephrin-A4	gi 183985625 gb BC166129.1	1297.844383
smad4	gi 54037962 gb BC084196.1	1053.601949
Cdx-2	gi 84105446 gb BC111473.1	600.0062069
Eukaryotic translation initiation factor 3 subunit 10	gi 35505403 gb BC057711.1	414.3164277
Churchill	gi 114107852 gb BC123207.1	369.3076365
pip4k2a	gi 120537387 gb BC129059.1	328.1431677
hnRNPK	gi 27882468 gb BC044711.1	319.4817015
MGC83026	gi 49118646 gb BC073670.1	226.469437
tpno2	gi 54673692 gb BC084978.1	222.1449285
nol12	gi 114107789 gb BC123345.1	151.6234281
epithelial V-like antigen 1	gi 50415563 gb BC077583.1	147.2011472
sfrs6	gi 28422194 gb BC044265.1	126.0892513
XIRG protein-like	gi 213623421 gb BC169722.1	87.788455
prickle1	gi 68533725 gb BC098954.1	83.19938866
ZFN384	gi 50415185 gb BC077403.1	69.76482898

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
RAC-beta serine/threonine-protein kinase B	gi 47939912 gb BC072041.1	62.12571541
ccb1-2	gi 30046518 gb BC051239.1	44.93558411
p80 katanin	gi 66910749 gb BC097654.1	40.55422632
zeb2	gi 54648610 gb BC084972.1	33.47771521
Zmiz1	gi 51513014 gb BC080428.1	30.23438945
Angiopoietin 4/5	gi 189442243 gb BC167504.1	27.19110778
HCF-1	gi 52138923 gb BC082658.1	26.78440995
CCR4-NOT transcription complex, subunit 10	gi 50416369 gb BC077237.1	21.48403283
fam107a/b MGC78851	gi 51261937 gb BC079918.1	21.17179772
Nucleoporin Seh1B MGC82845 protein	gi 49118558 gb BC073561.1	19.13482551
PI3K related SMG1 hypothetical protein MGC98890	gi 68226704 gb BC098320.1	17.94963894
Epsin-2 hypothetical protein MGC81482	gi 46249599 gb BC068837.1	16.4173713
srsf7	gi 50603926 gb BC077393.1	16.33581603
sf3b4	gi 28374169 gb BC045264.1	15.37049865
PPTC7 MGC81279 protein	gi 49257211 gb BC071109.1	13.98198898
meis3	gi 54673770 gb BC084920.1	13.07065969
origin recognition complex, subunit 6 homolog-like	gi 50603595 gb BC077746.1	13.01809093
DAXX ? hypothetical protein LOC446279	gi 86577707 gb BC112947.1	12.67764239
ACSL4 hypothetical protein LOC100174803	gi 189442239 gb BC167498.1	11.62060714
Necap2 MGC83534 protein	gi 50927256 gb BC079728.1	10.9853218
Timp3 tissue inhibitor of metalloproteinases-3	gi 38014484 gb BC060423.1	10.67580536
frizzled homolog 7	gi 27503170 gb BC042228.1	9.299494092
Serine/threonine/tyrosine-interacting protein B	gi 54311224 gb BC084791.1	9.188383287
UBADC1 hypothetical protein MGC115132	gi 62471528 gb BC093557.1	8.970846126

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
Cdea A7L transcription factor RAM2	gi 116487713 gb BC126014.1	8.574819986
Klf10 ? hypothetical protein MGC98877	gi 62089536 gb BC092147.1	7.695378855
ivns1abp influenza virus NS1A binding protein	gi 49898869 gb BC076641.1	7.664198955
MGC80567 protein	gi 50417996 gb BC077854.1	7.544735234
LCHN ? hypothetical protein MGC114999	gi 71050977 gb BC098994.1	7.224153034
RABGAP1L hypothetical protein MGC52980	gi 27694685 gb BC043775.1	7.11745345
PTN1 pleiotrophin MGC84465 protein	gi 49257697 gb BC074426.1	6.911246415
arrb1 arrestin, beta 1	gi 49904092 gb BC076815.1	6.832358987
Txnrd3 Thioredoxin reductase 2 MGC81848 protein	gi 51704105 gb BC081053.1	6.824096832
Foxi1 or Foxi4.2a fork head protein	gi 51258369 gb BC080044.1	6.805288292
LIMS1-b LIM domain hypothetical protein MGC81174	gi 47939771 gb BC072204.1	6.795291868
LMO7 LIM domain containing cDNA clone MGC:180040	gi 197245592 gb BC168520.1	6.755182581
arrdc3 arrestin containing hypothetical protein MGC131006	gi 80476391 gb BC108545.1	6.57050044
CANT1 Calcium activated nucleotidase similar to Ca <sup>2+</sup> -dependent endoplasmic reticulum nucleoside diphosphatase	gi 27370857 gb BC041215.1	6.486609662
D7 protein	gi 58702035 gb BC090198.1	6.413210477
Dact1 dapper 1 Antagonist of beta-catenin FRODO	gi 50418314 gb BC077380.1	6.403341734
RASSF7 Ras association domain containing MGC78972 protein	gi 84105479 gb BC111512.1	6.017970041
Sox11 XLS13B protein	gi 47124741 gb BC070707.1	5.989392572
Myt1 cDNA clone MGC:196991	gi 213626262 gb BC170264.1	5.974437792
zmiz2 MGC86475 protein	gi 51513014 gb BC080428.1	5.658053905
ZC3H7B zinc-finger CCCH-containing 7B MGC80522 protein	gi 50418254 gb BC077837.1	5.638059804
SAP130 HDAC MGC83894 protein	gi 50415582 gb BC077587.1	5.587991945

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
PCNA similar to proliferating cell nuclear antigen	gi 27371152 gb BC041549.1	5.340877685
Stx19 syntaxin 19 hypothetical LOC494752	gi 52354747 gb BC082852.1	5.239206209
HMG-box protein HMG2L1	gi 213625180 gb BC169998.1	5.171640761
Kif20a hypothetical LOC495414	gi 54648449 gb BC084922.1	5.055010856
slc7a3 solute carrier family 7 (cationic amino acid transporter, y <sup>+</sup> system), member 3	gi 27503399 gb BC042222.1	4.989471538
Lmo7 cDNA clone MGC:180040	gi 197245592 gb BC168520.1	4.861028301
Mark2 MAP/microtubule affinity-regulating kinase 2	gi 27694574 gb BC043730.1	4.821716572
Anp32b MGC80871 protein	gi 49118408 gb BC073408.1	4.77985399
cyclin A2	gi 50417439 gb BC077260.1	4.76329664
PPPDE2 peptidase domain containing MGC84710 protein	gi 49256350 gb BC074444.1	4.724302826
CTDP1 FCP1 serine phosphatase	gi 62185666 gb BC092306.1	4.712553945
ornithine decarboxylase-2	gi 28838468 gb BC047954.1	4.690222394
Ube2c hypothetical LOC496302	gi 57032917 gb BC088818.1	4.676640452
Efr3a MGC83628 protein	gi 51950039 gb BC082437.1	4.653269077
Dlg7 discs large hypothetical protein MGC116559	gi 68534624 gb BC099363.1	4.501586994
STXBP3 hypothetical protein MGC115462 syntaxin binding protein 3 (stxbp3)	gi 72679360 gb BC100235.1	4.472242676
Acy-3 aspartoacylase-3	gi 116487526 gb BC125990.1	4.452697089
PTDSS2 cDNA clone MGC:179871	gi 197246680 gb BC168517.1	4.234011971
Tcf-7 transcription factor 7 (T-cell specific, HMG-box)	gi 51261404 gb BC079972.1	4.200569032
lsp1 lymphocyte specific protein 1 hypothetical protein LOC100158340	gi 115528236 gb BC124864.1	4.124150256
NPHP3 nephronophthisis 3 MGC80264 protein	gi 50603779 gb BC077320.1	4.066245125
Med 15 Mediator complex subunit 15 ARC105 protein	gi 47123916 gb BC070536.1	4.029208683

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
cyclin E3	gi 58701930 gb BC090214.1	3.970372822
Fam60a hypothetical protein MGC115222	gi 66910763 gb BC097689.1	3.940864045
AHCTF1 AT hook containing transcription factor 1 MGC83673 protein	gi 49903664 gb BC076775.1	3.892143367
Rheb1 Ras homolog enriched in brain like 1 hypothetical LOC495056	gi 54037975 gb BC084211.1	3.882231045
RNF8a ring finger protein (C3HC4 type) 8	gi 28279439 gb BC046256.1	3.801782364
CCNT2 cyclin T2 MGC81210 protein	gi 51895950 gb BC081000.1	3.755306852
Tmed2 transmembrane emp24 domain trafficking protein 2 coated vesicle membrane protein, mRNA (cDNA clone MGC:52758 IMAGE:4684109	gi 28277265 gb BC044095.1	3.747391508
Mta1 metastatic associated 1 MGC83916 protein	gi 51950045 gb BC082445.1	3.743645989
MAPK8/Jnk1 mitogen-activated protein kinase 8	gi 28422153 gb BC046834.1	3.733178442
PSMD4 26S proteasome subunit	gi 66910701 gb BC097551.1	3.729782795
Poldip3 polymerase delta interaction protein 3 hypothetical protein MGC114944	gi 62471555 gb BC093543.1	3.720246762
DNAJC5B HSP cDNA clone MGC: 83536	gi 51703523 gb BC081115.1	3.720172358
NCBP2 Nuclear cap binding protein 2	gi 49117074 gb BC072902.1	3.701358817
FXDY FXDY domain containing ion transport	gi 125859119 gb BC129686.1	3.694185141
Ano5 Anoctamin 5 or Tmem16e	gi 50418049 gb BC077486.1	3.642280513
Not Annotated	gi 62739385 gb BC094151.1	3.628720112
Ttc30a tetratricopeptide repeat domain 30a	gi 47938700 gb BC072174.1	3.547737229
F2r11 Coagulation factor 2 receptor like 1	gi 57033014 gb BC088935.1	3.518659172
CSDA cols shock protein domain containing A	gi 161611734 gb BC155913.1	3.51654861
FUS Fused in Sarcoma?	gi 49522197 gb BC074437.1	3.505453855
Exo1 exonuclease 1	gi 54035217 gb BC084102.1	3.494289274
Cfp complement factor properdin	gi 50415018 gb BC077925.1	3.468804465

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
Ferritin light chain	gi 34785676 gb BC057216.1	3.464575104
cdc25c	gi 213626377 gb BC169346.1	3.456754005
SLC44a1 solute carrier family 44 member 1	gi 52354612 gb BC082837.1	3.306234736
PCF11 cleavage and poly-adenylation factor	gi 50414592 gb BC077233.1	3.277333059
Slc9a1 or NHE3 solute carrier family 9 member 3	gi 157422994 gb BC153791.1	3.274941479
Anks1a Ankyrin repeat and sterile alpha motif domain containing 1a	gi 47682305 gb BC070831.1	3.249886264
ap2b1 adaptor-related protein complex 1 beta 1 subunit	gi 120538239 gb BC129531.1	3.240669681
Not Annotated	gi 76780224 gb BC106027.1	3.21623043
Ctnnd1 Catenin (Cadherin associated protein) delta-1	gi 213623207 gb BC169434.1	3.210767484
GCAT Glycine C-acetyltransferase	gi 28704125 gb BC047258.1	3.210735376
beta arrestin	gi 49256118 gb BC072973.1	3.173896459
slc9a3r2	gi 55778573 gb BC086464.1	3.167840103
CTDP1 (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	gi 51950263 gb BC082378.1	3.162965383
MAX bHLH	gi 47123961 gb BC070710.1	3.144295944
MPV171	gi 51261416 gb BC079982.1	3.11285403
Fibronectin 1	gi 49114986 gb BC072841.1	3.110364743
Spicing factor (sfrs5)	gi 47717980 gb BC070967.1	3.1059201
transmembrane protein 45B	gi 120538262 gb BC129609.1	3.030355684
lysine (K)-specific demethylase 6A (kdm6a)	gi 50603932 gb BC077424.1	3.026903047
RalGDS/AF-6	gi 84105479 gb BC111512.1	2.963378492
Mek-2	gi 27694983 gb BC043913.1	2.955122189
calpain 2, (m/II) large subunit (capn2)	gi 39645066 gb BC063733.1	2.924548179
PHD finger protein 12 (phf12)	gi 46249573 gb BC068803.1	2.89562217
pax interacting (with transcription-activation domain) protein 1 (paxip1)	gi 50417566 gb BC077588.1	2.822971349

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
mediator complex subunit 16 (med16)	gi 62471580 gb BC093546.1	2.822152806
xRMD-2 microtubule-associated protein	gi 58702063 gb BC090235.1	2.803700074
tyrosine kinase 2 (tyk2)	gi 49118136 gb BC073112.1	2.790804764
methyltransferase like 3 (mettl3)	gi 46249483 gb BC068672.1	2.782222309
glycine amidinotransferase (L-arginine:glycine amidinotransferase) (gatm)	gi 28838491 gb BC047973.1	2.746369891
syntaxin 5 (stx5)	gi 76779222 gb BC106704.1	2.704962367
inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (ikkb)	gi 47939754 gb BC072192.1	2.686442963
G-2 and S-phase expressed 1 (gtse1)	gi 62471553 gb BC093540.1	2.683239948
RBL1	gi 47123210 gb BC070856.1	2.680418663
nucleoporin 93kDa (nup93)	gi 27924241 gb BC045089.1	2.672333338
embryonic ectoderm development (eed)	gi 50603665 gb BC077425.1	2.655016847
ring finger and CCCH-type domains 1 (rc3h1)	gi 46250191 gb BC068669.1	2.646867856
integrin, beta 5	gi 49899756 gb BC076844.1	2.636182901
ataxin 2 (atxn2)	gi 66910767 gb BC097692.1	2.634583223
chromosome 19 open reading frame 2 (c19orf2)	gi 50415135 gb BC077366.1	2.630865817
PRP4 pre-mRNA processing factor 4 homolog (prpf4)	gi 51703477 gb BC081044.1	2.62131998
protein phosphatase methylesterase 1 (ppme1)	gi 50418398 gb BC077600.1	2.617432826
orthodenticle homeobox 2 (otx2-a)	gi 50417481 gb BC077357.1	2.616883223
chromosome 13 open reading frame 34 (c13orf34)	gi 49523107 gb BC075159.1	2.599294339
DAZAP1	gi 50604139 gb BC077252.1	2.585999275
FSHD region gene 1 (frg1)	gi 49256477 gb BC074376.1	2.555875944
serine/threonine kinase 11 interacting protein (stk11ip)	gi 47682952 gb BC070809.1	2.553165597
carboxy-terminal kinesin 2	gi 54038135 gb BC084431.1	2.538623487
survival of motor neuron 2, centromeric (smn2)	gi 46249513 gb BC068721.1	2.535840144

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
sall1 (Sal-like 1)	gi 37590272 gb BC059284.1	2.505331347
NIMA (never in mitosis gene a)-related kinase 2 (nek2)	gi 27696903 gb BC043822.1	2.503175185
ZF-containing (posterior protein)	gi 213623475 gb BC169799.1	2.493496644
drebrin-like (dbnl)	gi 49257631 gb BC074277.1	2.479066307
jumonji domain containing 6 (jmd6-b)	gi 28277358 gb BC045252.1	2.4687995
inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (id3-a)	gi 27696824 gb BC044039.1	2.448101925
chaperonin containing TCP1, subunit 8 (theta) (cct8)	gi 67678231 gb BC097574.1	2.447348026
LIM domain containing preferred translocation partner in lipoma (lpp)	gi 62740239 gb BC094110.1	2.445439839
cytochrome c-1 (cyc1)	gi 71052231 gb BC099350.1	2.442233526
KIAA0182 (kiaa0182)	gi 120537359 gb BC129052.1	2.438699731
5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (atic)	gi 76779775 gb BC106381.1	2.42732299
ribonucleoprotein A1a (hnrnpa1)	gi 47938743 gb BC072090.1	2.419006697
caspase 3, apoptosis-related cysteine peptidase casp3	gi 68533747 gb BC098991.1	2.408087828
ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog) (ube2g1)	gi 28839012 gb BC047985.1	2.407955386
drebrin-like (dbnl)	gi 49257631 gb BC074277.1	2.388809202
PTK7 protein tyrosine kinase 7 (ptk7)	gi 148922111 gb BC146640.1	2.387741643
integrator complex subunit 2 (ints2)	gi 47125091 gb BC070524.1	2.387717766
PRP4 pre-mRNA processing factor 4 homolog B (prpf4b)	gi 125858002 gb BC129065.1	2.375801846
Transmembrane protein 33 (tmem33)	gi 49903380 gb BC076764.1	2.371301594
non-SMC condensin II complex, subunit D3 (ncapd3)	gi 49116983 gb BC073714.1	2.363179599
SIN3 homolog B, transcription regulator (sin3b)	gi 120538596 gb BC129063.1	2.353559822
splicing factor, arginine/serine-rich 18 (sfrs18)	gi 47940261 gb BC072160.1	2.350873591
mediator complex subunit 23 (med23)	gi 39645714 gb BC063725.1	2.349851184

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
phospholipase A2-activating protein (plaa)	gi 115528262 gb BC124847.1	2.344309729
minichromosome maintenance complex component 4 (mcm4-b)	gi 49115033 gb BC072870.1	2.342847336
NOP2/Sun domain family, member 2 (nsun2)	gi 66912075 gb BC097814.1	2.339817652
general transcription factor IIE, polypeptide 2, beta 34kDa (gtf2e2)	gi 58403335 gb BC089287.1	2.320004209
Rho GTPase activating protein 19 (arhgap19)	gi 48734660 gb BC072338.1	2.309370554
CCR4-NOT transcription complex, subunit 10 (cnot10-b)	gi 46250097 gb BC068748.1	2.298100702
lysine (K)-specific demethylase 3A (kdm3a-a)	gi 47506877 gb BC070982.1	2.296984096
zinc finger and BTB domain containing 44 (zbtb44)	gi 47124748 gb BC070714.1	2.293259115
phosphatidylinositol glycan anchor biosynthesis, class T (pigt)	gi 52354598 gb BC082818.1	2.284755462
heterogeneous nuclear ribonucleoprotein A3 (hnmpa3)	gi 213625122 gb BC169881.1	2.283526595
Putative ortholog of von Hippel-Lindau binding protein 1 (Prefoldin subunit 3)	gi 163916339 gb BC157499.1	2.278221284
nucleoporin 37kDa (nup37)	gi 51703531 gb BC081128.1	2.271537693
activating transcription factor 1 (ATF1)	gi 61403334 gb BC092037.1	2.266325959
Nedd4 family interacting protein 2 (ndfip2)	gi 50924805 gb BC079714.1	2.262854343
	gi 33416619 gb BC055957.1	2.260893298
proteasome (prosome, macropain) 26S subunit, ATPase, 3 (psmc3)	gi 28422358 gb BC046948.1	2.253753391
family with sequence similarity 109, member B (fam109b)	gi 47122977 gb BC070645.1	2.237428018
translation initiation factor 4E family member 3 (eif4e3-a)	gi 49257962 gb BC071126.1	2.230893103
ets variant gene 4	gi 50417509 gb BC077414.1	2.224884491
G kinase anchoring protein 1 (gkap1-a)	gi 49118875 gb BC073450.1	2.208726268
zinc finger transcription factor SALL4	gi 52138969 gb BC082637.1	2.190818022

<u>Gene</u>	<u>Clone ID</u>	<u>Fold Increase</u>
chromobox homolog 5 (cbx5)	gi 32766466 gb BC054962.1	2.18484743
CCR4-NOT transcription complex, subunit 6-like (cnot6l-a)	gi 47506927 gb BC071015.1	2.17052701
uridine-cytidine kinase 2 (uck2)	gi 52354745 gb BC082833.1	2.153018907
YY1 transcription factor (yy1-b)	gi 50925274 gb BC079731.1	2.144522678
karyopherin alpha 4 (importin alpha 3) (kpna4)	gi 47122818 gb BC070533.1	2.143067042
syntaxin 5 (stx5)	gi 76779222 gb BC106704.1	2.132374185
PRP4 pre-mRNA processing factor 4 homolog B (prpf4b)	gi 54038077 gb BC084355.1	2.120332678
oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) (ogdh)	gi 49118216 gb BC073213.1	2.110063412
acidic (leucine-rich) nuclear phosphoprotein 32 family, member B (anp32b)	gi 27503409 gb BC042250.1	2.104752746
AT hook containing transcription factor 1 (ahctf1)	gi 55250536 gb BC086281.1	2.095665156
proline-rich nuclear receptor coactivator 2 (pnrc2-b)	gi 54038003 gb BC084247.1	2.080782448
YY1 transcription factor	gi 50415555 gb BC077581.1	2.079401267
Ptk7	gi 38014809 gb BC060500.1	2.074966481
H3 histone, family 3B (H3.3B) (h3f3b)	gi 47506868 gb BC070966.1	2.05094159
bromodomain containing 1 (brd1)	gi 49118425 gb BC073421.1	2.046475407
mllt6	gi 52354628 gb BC082872.1	2.041361526
RAS oncogene family (rab18)	gi 33416685 gb BC056054.1	2.03028667
RAB6A, member RAS oncogene family (rab6a)	gi 28302337 gb BC046683.1	2.027277987
transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) (tcf3)	gi 28422165 gb BC046840.1	2.026584776
cell division cycle 20 homolog (cdc20)	gi 50370183 gb BC076805.1	2.012178568
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (sema6d)	gi 213626595 gb BC169687.1	2.010828849
lethal giant larvae homolog 1 (llg1)	gi 47123133 gb BC070788.1	2.000831812